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Rates of nuclear and cytoplasmic mitochondrial DNA sequence divergence in mammals.

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Differential rates of nucleotide substitution among different gene segments and between distinct evolutionary lineages is well documented among mitochondrial genes and is likely a consequence of locus-specific selective constraints that delimit mutational divergence over evolutionary time. We compared sequence variation of 18 homologous loci (15 coding genes and 3 parts of the control region) among 10 mammalian mitochondrial DNA genomes which allowed us to describe different mitochondrial evolutionary patterns and to produce an estimation of the relative order of gene divergence. The relative rates of divergence of mitochondrial DNA genes in the family Felidae were estimated by comparing their divergence from homologous counterpart genes included in nuclear mitochondrial DNA (Numt, pronounced "new might"), a genomic fossil that represents an ancient transfer of 7.9 kb of mitochondrial DNA to the nuclear genome of an ancestral species of the domestic cat (*Felis catus*). Phylogenetic analyses of mitochondrial (mtDNA) sequences with multiple outgroup species were conducted to date the ancestral node common to the Numt and the cytoplasmic (Cymt) mtDNA genes and to calibrate the rate of sequence divergence of mitochondrial genes relative to nuclear homologous counterparts. By setting the fastest substitution rate as strictly mutational, an empirical "selective retardation index" is computed to quantify the sum of all constraints, selective and otherwise, that limit sequence divergence of mitochondrial gene sequences over time.

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